SEQUENCE LISTING

<110> ABBOTT, Catherine Anne
GORRELL, Mark Douglas

<120> DIPEPTIDYL PEPTIDASES

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<150> PCT/AU00/01085
<151> 2000-09-11

<150> AU PQ5709
<151> 2000-02-18

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<151> 1999-09-10

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<210> 1
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<212> PRT
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<400> 1

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Glu Pro Phe Tyr Val Glu Arg Tyr Ser Trp Ser Gln Leu Lys Lys Leu
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Leu Ala Asp Thr Arg Lys Tyr His Gly Tyr Met Met Ala Lys Ala Pro
    50                  55                  60
His Asp Phe Met Phe Val Lys Arg Asn Asp Pro Asp Gly Pro His Ser
65                  70                  75                  80
Asp Arg Ile Tyr Tyr Leu Ala Met Ser Gly Glu Asn Arg Glu Asn Thr
                85                  90                  95
Leu Phe Tyr Ser Glu Ile Pro Lys Thr Ile Asn Arg Ala Ala Val Leu
            100                 105                 110
Met Leu Ser Trp Lys Pro Val Leu Asp Val Phe Glu Ala Thr Leu Asp
        115                 120                 125
Tyr Gly Met Tyr Ser Arg Glu Glu Glu Leu Leu Arg Glu Arg Lys Arg
    130                 135                 140
Ile Gly Thr Val Gly Ile Ala Ser Tyr Asp Tyr His Gln Gly Ser Gly
145                 150                 155                 160
Thr Phe Leu Phe Gln Ala Gly Ser Gly Ile Tyr His Val Lys Asp Gly
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Gly Pro Gln Gly Phe Thr Gln Gln Pro Leu Arg Pro Asn Leu Val Glu
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Thr Ser Cys Pro Asn Ile Arg Met Asp Pro Lys Leu Cys Pro Ala Asp
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225                 230                 235                 240
Ala Asn Met Glu Glu Asp Ala Arg Ser Ala Gly Val Ala Thr Phe Val
                245                 250                 255
Leu Gln Glu Glu Phe Asp Arg Tyr Ser Gly Tyr Trp Trp Cys Pro Lys
            260                 265                 270
Ala Glu Thr Thr Pro Ser Gly Gly Lys Ile Leu Arg Ile Leu Tyr Glu
        275                 280                 285
Glu Asn Asp Glu Ser Glu Val Glu Ile Ile His Val Thr Ser Pro Met
    290                 295                 300
Leu Glu Thr Arg Arg Ala Asp Ser Phe Arg Tyr Pro Lys Thr Gly Thr
305                 310                 315                 320
Ala Asn Pro Lys Val Thr Phe Lys Met Ser Glu Ile Met Ile Asp Ala
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Glu Gly Arg Ile Ile Asp Val Ile Asp Lys Glu Leu Ile Gln Pro Phe
            340                 345                 350
Glu Ile Leu Phe Glu Gly Val Glu Tyr Ile Ala Arg Ala Gly Trp Thr
        355                 360                 365
Pro Glu Gly Lys Tyr Ala Trp Ser Ile Leu Leu Asp Arg Ser Gln Thr
    370                 375                 380
Arg Leu Gln Ile Val Leu Ile Ser Pro Glu Leu Phe Ile Pro Val Glu
385                 390                 395                 400
Asp Asp Val Met Glu Arg Gln Arg Leu Ile Glu Ser Val Pro Asp Ser
                405                 410                 415
Val Thr Pro Leu Ile Ile Tyr Glu Glu Thr Thr Asp Ile Trp Ile Asn
            420                 425                 430
Ile His Asp Ile Phe His Val Phe Pro Gln Ser His Glu Glu Glu Ile
        435                 440                 445
Glu Phe Ile Phe Ala Ser Glu Cys Lys Thr Gly Phe Arg His Leu Tyr
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Lys Ile Thr Ser Ile Leu Lys Glu Ser Lys Tyr Lys Arg Ser Ser Gly
465                 470                 475                 480
Gly Leu Pro Ala Pro Ser Asp Phe Lys Cys Pro Ile Lys Glu Glu Ile
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Ala Ile Thr Ser Gly Glu Trp Glu Val Leu Gly Arg His Gly Ser Asn
            500                 505                 510
Ile Gln Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu Gly Thr Lys
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Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr Val Asn Pro
    530                 535                 540
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545                 550                 555                 560
Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser Asn Gln Lys
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Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro Glu Asp Asp
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Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu Asp Ser Ala
        595                 600                 605
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Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro His Asp Leu
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Gln Val Gln Leu Val Asn Asn Arg Phe Lys Gly Val Lys Tyr Phe Arg
660 665 670
Leu Asn Thr Leu Ala Ser Leu Gly Tyr Val Val Val Val Ile Asp Asn
675 680 685
Arg Gly Ser Cys His Arg Gly Leu Lys Phe Glu Gly Ala Phe Lys Tyr
690 695 700
Lys Met Gly Gln Ile Glu Ile Asp Asp Gln Val Glu Gly Leu Gln Tyr
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725 730 735
Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala Leu Met Gln Arg
740 745 750
Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp
755 760 765
Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met Gly His Pro Asp
770 775 780
Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala Met Gln Ala Glu
785 790 795 800
Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu His Gly Phe Leu
805 810 815
Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu Leu Ser Phe Leu
820 825 830
Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr Pro Gln Glu Arg
835 840 845
His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr Glu Leu His Leu
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Leu His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile Ala Ala Leu Lys
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<212> DNA
<213> Homo Sapiens

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<212> PRT
<213> Homo Sapiens

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        35                  40                  45
Tyr Ser Asn Gln Lys Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser
    50                  55                  60
Ser Pro Glu Asp Asp Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr
65                  70                  75                  80
Ile Leu Asp Ser Ala Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile
                85                  90                  95
Phe Ser Phe Glu Ser Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr
            100                 105                 110
Lys Pro His Asp Leu Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe
        115                 120                 125
Ile Tyr Gly Gly Pro Gln Gly Gln Ile Glu Ile Asp Asp Gln Val Glu
    130                 135                 140
Gly Leu Gln Tyr Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg
145                 150                 155                 160
Val Gly Ile His Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala
                165                 170                 175
Leu Met Gln Arg Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro
            180                 185                 190
Val Thr Leu Trp Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met
        195                 200                 205
Gly His Pro Asp Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala
    210                 215                 220
Met Gln Ala Glu Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu
225                 230                 235                 240
His Gly Phe Leu Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu
                245                 250                 255
Leu Ser Phe Leu Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr
            260                 265                 270
Pro Gln Glu Arg His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr
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<211> 1197
<212> DNA
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<212> PRT
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Gln Pro Phe Glu Ile Leu Phe Glu Gly Val Glu Tyr Ile Ala Arg Ala
        35   40   45
Gly Trp Thr Pro Glu Gly Lys Tyr Ala Trp Ser Ile Leu Leu Asp Arg
    50   55   60
Ser Gln Thr Arg Leu Gln Ile Val Leu Ile Ser Pro Glu Leu Phe Ile
65   70   75   80
Pro Val Glu Asp Asp Val Met Glu Arg Gln Arg Leu Ile Glu Ser Val
                85   90   95
Pro Asp Ser Val Thr Pro Leu Ile Ile Tyr Glu Glu Thr Thr Asp Ile
            100   105   110
Trp Ile Asn Ile His Asp Ile Phe His Val Phe Pro Gln Ser His Glu
        115   120   125
Glu Glu Ile Glu Phe Ile Phe Ala Ser Glu Cys Lys Thr Gly Phe Arg
    130   135   140
His Leu Tyr Lys Ile Thr Ser Ile Leu Lys Glu Ser Lys Tyr Lys Arg
145   150   155   160
Ser Ser Gly Gly Leu Pro Ala Pro Ser Asp Phe Lys Cys Pro Ile Lys
                165   170   175
Glu Glu Ile Ala Ile Thr Ser Glu Glu Trp Glu Val Leu Gly Arg His
            180   185   190
Gly Ser Asn Ile Gln Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu
        195   200   205
Gly Thr Lys Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr
    210   215   220
Val Asn Pro Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr Ser His
225   230   235   240
Ser Cys Cys Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser
                245   250   255
Asn Gln Lys Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro

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            260                 265                 270
Glu Asp Asp Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu
        275                 280                 285
Asp Ser Ala Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser
    290                 295                 300
Phe Glu Ser Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro
305                 310                 315                 320
His Asp Leu Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr
                325                 330                 335
Gly Gly Pro Gln Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp Ile
            340                 345                 350
Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met Gly His Pro Asp Gln
        355                 360                 365
Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala Met Gln Ala Glu Lys
    370                 375                 380
Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu His Gly Phe Leu Asp
385                 390                 395                 400
Glu Asn Val His Phe Ala His Thr Ser Ile Leu Leu Ser Phe Leu Val
                405                 410                 415
Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr Pro Gln Glu Arg His
            420                 425                 430
Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr Glu Leu His Leu Leu
        435                 440                 445
His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile Ala Ala Leu Lys Val
    450                 455                 460
Ile
465
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<211> 1669
<212> DNA
<213> Homo Sapiens

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<211> 360
<212> PRT
<213> Homo Sapiens

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35 40 45
Glu Ser Glu Val Glu Ile Ile His Val Thr Ser Pro Met Leu Glu Thr
50 55 60
Arg Arg Ala Asp Ser Phe Arg Tyr Pro Lys Thr Gly Thr Ala Asn Pro
65 70 75 80
Lys Val Thr Phe Lys Met Ser Glu Ile Met Ile Asp Ala Glu Gly Arg
85 90 95
Ile Ile Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu Gly Thr Lys
100 105 110
Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr Val Asn Pro
115 120 125
Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr Ser His Ser Cys Cys
130 135 140
Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser Asn Gln Lys
145 150 155 160
Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro Glu Asp Asp
165 170 175
Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu Asp Ser Ala
180 185 190
Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser Phe Glu Ser
195 200 205
Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro His Asp Leu
210 215 220
Gln Pro Gln Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr Gly Gly Pro
225 230 235 240
Gln Val Gln Leu Val Asn Asn Arg Phe Lys Gly Val Lys Tyr Phe Arg
245 250 255
Leu Asn Thr Leu Ala Ser Leu Gly Tyr Val Val Val Val Ile Asp Asn
260 265 270
Arg Gly Ser Cys His Arg Gly Leu Lys Phe Glu Gly Ala Phe Lys Tyr
275 280 285

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Lys Met Gly Gln Ile Glu Ile Asp Asp Gln Val Glu Gly Leu Gln Tyr
    290                 295                 300
Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg Val Gly Ile His
305                 310                 315                 320
Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala Leu Met Gln Arg
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Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp
            340                 345                 350
Ile Phe Tyr Asp Thr Gly Tyr Thr
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<210> 8
<211> 1083
<212> DNA
<213> Homo Sapiens

<400> 8

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tatgttggaa acaaggaggg cagattcatt ccgttatcct aaaacaggta cagcaaatcc 240
taaagtcact tttaagatgt cagaaataat gattgatgct gaaggaagga tcatagttga 300
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